

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/008,264C
Source: IFW16
Date Processed by STIC: 1/31/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/008,264C

CRF Edit Date: 2/3/06
Edited by: M

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

 Deleted:  invalid beginning/end-of-file text ; page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

— Other:



IFW16

RAW SEQUENCE LISTING DATE: 02/03/2006
 PATENT APPLICATION: US/10/008,264C TIME: 12:53:58

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF4\02032006\J008264C.raw

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4 <110> APPLICANT: Glimcher, Laurie H.
5   Szabo, Susanne, J.
7 <120> TITLE OF INVENTION: T-BET COMPOSITIONS AND METHODS OF USE THEREOF
9 <130> FILE REFERENCE: HUI-040CP
11 <140> CURRENT APPLICATION NUMBER: US 10/008264C
12 <141> CURRENT FILING DATE: 2001-12-03
14 <150> PRIOR APPLICATION NUMBER: PCT/US00/15345
15 <151> PRIOR FILING DATE: 2000-06-01
17 <150> PRIOR APPLICATION NUMBER: US 60/137085
18 <151> PRIOR FILING DATE: 1999-06-02
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1608
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
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38 ccg atg ccg ggg agc gac gag ggc cgg gcg cct ggc gcc gac ccg cag      96
39 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
40       20          25          30
42 cac cgc tac ttc tac ccg gag ccg ggc gcg cag gac gac gag cgt      144
43 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
44       35          40          45
46 cgc ggg ggc ggc agc ctg ggg tct ccc tac ccg ggg ggc gcc ttg gtg     192
47 Arg Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
48       50          55          60
50 ccc gcc ccg ccg agc cgc ttc ctt gga gcc tac gcc tac ccg ccg cga     240
51 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
52   65          70          75          80
54 ccc cag ggc ggc ttc ccc ggc gcg ggc gag tcc ttc ccg ccg ccc     288
55 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
56       85          90          95
58 gcg gac gcc gag ggc tac cag ccg ggc gag ggc tac gcc gcc ccg gac     336
59 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
60       100         105         110
63 ccg cgc gcc ggg ctc tac ccg ggg ccg cgt gag gac tac gcg cta ccc     384
64 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro

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67	gca gga ctg gag gtg tcg ggg aaa	ctg agg gtc gcg ctc aac aac cac		432
68	Ala Gly Leu Glu Val Ser Gly Lys	Leu Arg Val Ala Leu Asn Asn His		
69	130	135	140	
71	ctg ttg tgg tcc aag ttt aat cag cac cag aca gag atg atc atc acc			480
72	Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr			
73	145	150	155	160
75	aag cag gga cgg cgg atg ttc cca ttc ctg tca ttt act gtg gcc ggg			528
76	Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly			
77	165	170	175	
79	ctg gag ccc acc agc cac tac agg atg ttt gtg gac gtg gtc ttg gtg			576
80	Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val			
81	180	185	190	
83	gac cag cac cac tgg cgg tac cag agc ggc aag tgg gtg cag tgt gga			624
84	Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly			
85	195	200	205	
87	aag gcc gag ggc agc atg cca gga aac cgc ctg tac gtc cac ccg gac			672
88	Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp			
89	210	215	220	
91	tcc ccc aac aca gga gcg cac tgg atg cgc cag gaa gtt tca ttt ggg			720
92	Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly			
93	225	230	235	240
95	aaa cta aag ctc aca aac aag ggg gcg tcc aac aat gtg acc cag			768
96	Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln			
97	245	250	255	
99	atg att gtg ctc cag tcc ctc cat aag tac cag ccc cgg ctg cat atc			816
100	Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile			
101	260	265	270	
103	gtt gag gtg aac gac gga gag cca gag gca gcc tgc aac gct tcc aac			864
104	Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn			
105	275	280	285	
107	acg cat atc ttt act ttc caa gaa acc cag ttc att gcc gtg act gcc			912
108	Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala			
109	290	295	300	
111	tac cag aat gcc gag att act cag ctg aaa att gat aat aac ccc ttt			960
112	Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe			
113	305	310	315	320
115	gcc aaa gga ttc cgg gag aac ttt gag tcc atg tac aca tct gtt gac			1008
116	Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp			
117	325	330	335	
119	acc agc atc ccc tcc cgg cct gga ccc aac tgt caa ttc ctt ggg gga			1056
120	Thr Ser Ile Pro Ser Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly			
121	340	345	350	
124	gat cac tac tct ctc cta ccc aac cag tat cct gtt ccc agc cgc			1104
125	Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg			
126	355	360	365	
128	tcc tac ccc gac ctt cct ggc cag gcg aag gat gtg gtt ccc cag gct			1152
129	Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala			
130	370	375	380	

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Input Set : A:\PTO.AMC.txt
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132	tac tgg ctg ggg gcc ccc cg	gac cac agc tat gag gct gag ttt cga	1200	
133	Tyr Trp Leu Gly Ala Pro Arg	Asp His Ser Tyr Glu Ala Glu Phe Arg		
134	385	390	395	400
136	gca gtc agc atg aag cct gca	ttc ttg ccc tct gcc cct ggg ccc acc	1248	
137	Ala Val Ser Met Lys Pro Ala	Phe Leu Pro Ser Ala Pro Gly Pro Thr		
138	405	410	415	
140	atg tcc tac tac cga ggc cag	gag gtc ctg gca cct gga gct ggc tgg	1296	
141	Met Ser Tyr Tyr Arg Gly Gln	Glu Val Leu Ala Pro Gly Ala Gly Trp		
142	420	425	430	
144	cct gtg gca ccc cag tac cct	ccc aag atg ggc ccg gcc agc tgg ttc	1344	
145	Pro Val Ala Pro Gln Tyr Pro	Pro Lys Met Gly Pro Ala Ser Trp Phe		
146	435	440	445	
148	cgc cct atg cgg act ctg ccc	atg gaa ccc ggc cct gga ggc tca gag	1392	
149	Arg Pro Met Arg Thr Leu Pro	Met Glu Pro Gly Pro Gly Ser Glu		
150	450	455	460	
152	gga cgg gga cca gag gac	cag ggt ccc ccc ttg gtg tgg act gag att	1440	
153	Gly Arg Gly Pro Glu Asp Gln	Gly Pro Pro Leu Val Trp Thr Glu Ile		
154	465	470	475	480
156	gcc ccc atc cgg ccg gaa tcc	agt gat tca gga ctg ggc gaa gga gac	1488	
157	Ala Pro Ile Arg Pro Glu Ser	Ser Asp Ser Gly Leu Gly Glu Gly Asp		
158	485	490	495	
160	tct aag agg agg cgc gtg	tcc ccc tat cct tcc agt ggt gac agc tcc	1536	
161	Ser Lys Arg Arg Val Ser Pro	Tyr Pro Ser Ser Gly Asp Ser Ser		
162	500	505	510	
164	tcc cct gct ggg gcc cct	tct ttt gat aag gaa gct gaa gga cag	1584	
165	Ser Pro Ala Gly Ala Pro Ser	Pro Phe Asp Lys Glu Ala Glu Gly Gln		
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173	<210> SEQ ID NO: 2			
174	<211> LENGTH: 535			
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176	<213> ORGANISM: Homo sapiens			
178	<400> SEQUENCE: 2			
179	Met Gly Ile Val Glu Pro Gly Cys	Gly Asp Met Leu Thr Gly Thr Glu		
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182	Pro Met Pro Gly Ser Asp Glu	Gly Arg Ala Pro Gly Ala Asp Pro Gln		
183	20	25	30	
185	His Arg Tyr Phe Tyr Pro Glu	Pro Gly Ala Gln Asp Ala Asp Glu Arg		
186	35	40	45	
188	Arg Gly Gly Ser Leu Gly Ser	Pro Tyr Pro Gly Gly Ala Leu Val		
189	50	55	60	
191	Pro Ala Pro Pro Ser Arg Phe	Leu Gly Ala Tyr Ala Tyr Pro Pro Arg		
192	65	70	75	80
194	Pro Gln Ala Ala Gly Phe	Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro		
195	85	90	95	
197	Ala Asp Ala Glu Gly Tyr Gln	Pro Gly Glu Gly Tyr Ala Ala Pro Asp		
198	100	105	110	

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Input Set : A:\PTO.AMC.txt
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200 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro
201 115 120 125
203 Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His
204 130 135 140
206 Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr
207 145 150 155 160
209 Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly
210 165 170 175
212 Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val
213 180 185 190
215 Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly
216 195 200 205
218 Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp
219 210 215 220
221 Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly
222 225 230 235 240
224 Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln
225 245 250 255
227 Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile
228 260 265 270
230 Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn
231 275 280 285
233 Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala
234 290 295 300
236 Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe
237 305 310 315 320
239 Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp
240 325 330 335
242 Thr Ser Ile Pro Ser Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly
243 340 345 350
246 Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg
247 355 360 365
249 Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala
250 370 375 380
252 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
253 385 390 395 400
255 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
256 405 410 415
258 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
259 420 425 430
261 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
262 435 440 445
264 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Ser Glu
265 450 455 460
267 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
268 465 470 475 480
270 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
271 485 490 495
273 Ser Lys Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser

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DATE: 02/03/2006
TIME: 12:53:58

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02032006\J008264C.raw

274	500	505	510	
276	Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln			
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288	<220> FEATURE:			
289	<221> NAME/KEY: CDS			
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295	1 5 10 15			
297	ccg atg ccg agt gac gag ggc cgg ggg ccc gga gcg gac caa cag cat	96		
298	Pro Met Pro Ser Asp Glu Gly Arg Gly Pro Gly Ala Asp Gln Gln His			
299	20 25 30			
302	cgt ttc ttc tat ccc gag ccg ggc gca cag gac ccg acc gat cgc cgc	144		
303	Arg Phe Phe Tyr Pro Glu Pro Gly Ala Gln Asp Pro Thr Asp Arg Arg			
304	35 40 45			
306	gca ggt agc agc ctg ggg acg ccc tac tct ggg ggc gcc ctg gtg cct	192		
307	Ala Gly Ser Ser Leu Gly Thr Pro Tyr Ser Gly Gly Ala Leu Val Pro			
308	50 55 60			
310	gcc gcg ccg ggt cgc ttc ctt gga tcc ttc gcc tac ccg ccc cgg gct	240		
311	Ala Ala Pro Gly Arg Phe Leu Gly Ser Phe Ala Tyr Pro Pro Arg Ala			
312	65 70 75 80			
314	cag gtg gct ggc ttt ccc ggg cct ggc gag ttc ttc ccg ccg ccc gcg	288		
315	Gln Val Ala Gly Phe Pro Gly Pro Gly Glu Phe Phe Pro Pro Pro Ala			
316	85 90 95			
318	ggt gcg gag ggc tac ccg ccc gtg gat ggc tac cct gcc cct gac ccg	336		
319	Gly Ala Glu Gly Tyr Pro Pro Val Asp Gly Tyr Pro Ala Pro Asp Pro			
320	100 105 110			
322	cgc gcg ggg ctc tac cca ggg ccg cgc gag gac tac gca ttg ccc gcg	384		
323	Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro Ala			
324	115 120 125			
326	ggg ttg gag gtg tct ggg aag ctg aga gtc gcg ctc agc aac cac ctg	432		
327	Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Ser Asn His Leu			
328	130 135 140			
330	ttg tgg tcc aag ttc aac cag cac cag aca gag atg atc atc act aag	480		
331	Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr Lys			
332	145 150 155 160			
334	caa gga cgg cga atg ttc cca ttc ctg tcc ttc acc gtg gcc ggg ctg	528		
335	Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly Leu			
336	165 170 175			
338	gag ccc aca agc cat tac agg atg ttt gtg gat gtg gtc ttg gtg gac	576		
339	Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val Asp			
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/008,264C

DATE: 02/03/2006

TIME: 12:53:59

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02032006\J008264C.raw

Raw Sequence Listing before editing (for reference only)



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/008,264C

DATE: 01/31/2006
TIME: 10:59:35

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\01312006\J008264C.raw

4 <110> APPLICANT: Glimcher, Laurie H.
 5 Szabo, Susanne, J.
 7 <120> TITLE OF INVENTION: T-BET COMPOSITIONS AND METHODS OF USE THEREOF
 9 <130> FILE REFERENCE: HUI-040CP
 11 <140> CURRENT APPLICATION NUMBER: US 10/008264C
 12 <141> CURRENT FILING DATE: 2001-12-03
 14 <150> PRIOR APPLICATION NUMBER: PCT/US00/15345
 15 <151> PRIOR FILING DATE: 2000-06-01
 17 <150> PRIOR APPLICATION NUMBER: US 60/137085
 18 <151> PRIOR FILING DATE: 1999-06-02
 20 <160> NUMBER OF SEQ ID NOS: 9
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1608
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
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 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1605)
 33 <400> SEQUENCE: 1
 34 atg ggc atc gtg gag ccg ggt tgc gga gac atg ctg acg ggc acc gag 48
 35 Met Gly Ile Val Glu Pro Gly Cys Gly Asp Met Leu Thr Gly Thr Glu
 36 1 5 10 15
 38 ccg atg ccg ggg agc gac gag ggc cgg gcg cct ggc gcc gac ccg cag 96
 39 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
 40 20 25 30
 42 cac cgc tac ttc tac ccg gag ccg ggc gcg cag gac gac gag cgt 144
 43 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
 44 35 40 45
 46 cgc ggg ggc agc ctg ggg tct ccc tac ccg ggg ggc gcc ttg gtg 192
 47 Arg Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
 48 50 55 60
 50 ccc gcc ccg ccg agc cgc ttc ctt gga gcc tac gcc tac ccg ccg cga 240
 51 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
 52 65 70 75 80
 54 ccc cag gcg gcc ggc ttc ccc ggc gcg ggc gag tcc ttc ccg ccg ccc 288
 55 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
 56 85 90 95
 58 gcg gac gcc gag ggc tac cag ccg ggc gag ggc tac gcc gcc ccg gac 336
 59 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
 60 100 105 110
 63 ccg cgc gcc ggg ctc tac ccg ggg ccg cgt gag gac tac gcg cta ccc 384
 64 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro

P.6
Does Not Comply
Corrected Diskette Needed

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65	115	120	125	
67	gca ggc ctg gag gtg tcg ggg aaa ctg agg gtc gcg ctc aac aac cac			432
68	Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His			
69	130	135	140	
71	ctg ttg tgg tcc aag ttt aat cag cac cag aca gag atg atc atc acc			480
72	Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr			
73	145	150	155	160
75	aag cag gga cgg cgg atg ttc cca ttc ctg tca ttt act gtg gcc ggg			528
76	Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly			
77	165	170	175	
79	ctg gag ccc acc agc cac tac agg atg ttt gtg gac gtg gtc ttg gtg			576
80	Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val			
81	180	185	190	
83	gac cag cac cac tgg cgg tac cag agc ggc aag tgg gtg cag tgt gga			624
84	Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly			
85	195	200	205	
87	aag gcc gag ggc agc atg cca gga aac cgc ctg tac gtc cac ccg gac			672
88	Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp			
89	210	215	220	
91	tcc ccc aac aca gga gcg cac tgg atg cgc cag gaa gtt tca ttt ggg			720
92	Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly			
93	225	230	235	240
95	aaa cta aag ctc aca aac aac aag ggg gcg tcc aac aat gtg acc cag			768
96	Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln			
97	245	250	255	
99	atg att gtg ctc cag tcc ctc cat aag tac cag ccc cgg ctg cat atc			816
100	Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile			
101	260	265	270	
103	gtt gag gtg aac gac gga gag cca gag gca gcc tgc aac gct tcc aac			864
104	Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn			
105	275	280	285	
107	acg cat atc ttt act ttc caa gaa acc cag ttc att gcc gtg act gcc			912
108	Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala			
109	290	295	300	
111	tac cag aat gcc gag att act cag ctg aaa att gat aat aac ccc ttt			960
112	Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe			
113	305	310	315	320
115	gcc aaa gga ttc cgg gag aac ttt gag tcc atg tac aca tct gtt gac			1008
116	Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp			
117	325	330	335	
119	acc agc atc ccc tcc ccg cct gga ccc aac tgt caa ttc ctt ggg gga			1056
120	Thr Ser Ile Pro Ser Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly			
121	340	345	350	
124	gat cac tac tct ctc cta ccc aac cag tat cct gtt ccc agc cgc			1104
125	Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg			
126	355	360	365	
128	tcc tac ccc gac ctt cct ggc cag gcg aag gat gtg gtt ccc cag gct			1152
129	Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala			
130	370	375	380	

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138 405 410 415	
140 atg tcc tac tac cga ggc cag gag gtc ctg gca cct gga gct ggc tgg	1296
141 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp	
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146 435 440 445	
148 cgc cct atg cgg act ctg ccc atg gaa ccc ggc cct gga ggc tca gag	1392
149 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu	
150 450 455 460	
152 gga cgg gga cca gag gac cag ggt ccc ccc ttg gtg tgg act gag att	1440
153 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile	
154 465 470 475 480	
156 gcc ccc atc cgg cc ^g gaa tcc agt gat tca gga ctg ggc gaa gga gac	1488
157 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp	
158 485 490 495	
160 tct aag agg agg cgc gtg tcc ccc tat cct tcc agt ggt gac agc tcc	1536
161 Ser Lys Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser	
162 500 505 510	
164 tcc cct gct ggg gcc cct tct cct ttt gat aag gaa gct gaa gga cag	1584
165 Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln	
166 515 520 525	
168 ttt tat aac tat ttt ccc aac tga	1608
169 Phe Tyr Asn Tyr Phe Pro Asn	
170 530 535	
173 <210> SEQ ID NO: 2	
174 <211> LENGTH: 535	
175 <212> TYPE: PRT	
176 <213> ORGANISM: Homo sapiens	
178 <400> SEQUENCE: 2	
179 Met Gly Ile Val Glu Pro Gly Cys Gly Asp Met Leu Thr Gly Thr Glu	
180 1 5 10 15	
182 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln	
183 20 25 30	
185 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg	
186 35 40 45	
188 Arg Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val	
189 50 55 60	
191 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg	
192 65 70 75 80	
194 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro	
195 85 90 95	
197 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp	
198 100 105 110	

RAW SEQUENCE LISTING
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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\01312006\J008264C.raw

200 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro
 201 115 120 125
 203 Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His
 204 130 135 140
 206 Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr
 207 145 150 155 160
 209 Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly
 210 165 170 175
 212 Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val
 213 180 185 190
 215 Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly
 216 195 200 205
 218 Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp
 219 210 215 220
 221 Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly
 222 225 230 235 240
 224 Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln
 225 245 250 255
 227 Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile
 228 260 265 270
 230 Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn
 231 275 280 285
 233 Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala
 234 290 295 300
 236 Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe
 237 305 310 315 320
 239 Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp
 240 325 330 335
 242 Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly
 243 340 345 350
 246 Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg
 247 355 360 365
 249 Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala
 250 370 375 380
 252 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
 253 385 390 395 400
 255 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
 256 405 410 415
 258 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
 259 420 425 430
 261 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
 262 435 440 445
 264 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
 265 450 455 460
 267 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
 268 465 470 475 480
 270 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
 271 485 490 495
 273 Ser Lys Arg Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser

RAW SEQUENCE LISTING
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Input Set : A:\SEQUENCE LISTING.txt
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274	500	505	510
276	Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln		
277	515	520	525
279	Phe Tyr Asn Tyr Phe Pro Asn		
280	530	535	
283	<210> SEQ ID NO: 3		
284	<211> LENGTH: 1593		
285	<212> TYPE: DNA		
286	<213> ORGANISM: Mus musculus		
288	<220> FEATURE:		
289	<221> NAME/KEY: CDS		
290	<222> LOCATION: (1)..(1590)		
292	<400> SEQUENCE: 3		
293	atg ggc atc gtg gag ccg ggc tgc gga gac atg ctg acc ggc acc gag	48	
294	Met Gly Ile Val Glu Pro Gly Cys Gly Asp Met Leu Thr Gly Thr Glu		
295	1 5 10 15		
297	ccg atg ccg agt gac gag ggc ccg ggg ccc gga gcg gac caa cag cat	96	
298	Pro Met Pro Ser Asp Glu Gly Arg Gly Pro Gly Ala Asp Gln Gln His		
299	20 25 30		
302	cgt ttc ttc tat ccc gag ccg ggc gca cag gac ccg acc gat cgc cgc	144	
303	Arg Phe Phe Tyr Pro Glu Pro Gly Ala Gln Asp Pro Thr Asp Arg Arg		
304	35 40 45		
306	gca ggt agc agc ctg ggg acg ccc tac tct ggg ggc gcc ctg gtg cct	192	
307	Ala Gly Ser Ser Leu Gly Thr Pro Tyr Ser Gly Gly Ala Leu Val Pro		
308	50 55 60		
310	gcc gcg ccg ggt cgc ttc ctt gga tcc ttc gcc tac ccg ccc cgg gct	240	
311	Ala Ala Pro Gly Arg Phe Leu Gly Ser Phe Ala Tyr Pro Pro Arg Ala		
312	65 70 75 80		
314	cag gtg gct ggc ttt ccc ggg cct ggc gag ttc ttc ccg ccg ccc gcg	288	
315	Gln Val Ala Gly Phe Pro Gly Pro Gly Glu Phe Phe Pro Pro Pro Ala		
316	85 90 95		
318	ggt gcg gag ggc tac ccg ccc gtg gat ggc tac cct gcc cct gac ccg	336	
319	Gly Ala Glu Gly Tyr Pro Pro Val Asp Gly Tyr Pro Ala Pro Asp Pro		
320	100 105 110		
322	cgc gcg ggg ctc tac cca ggg ccg cgc gag gac tac gca ttg ccc gcg	384	
323	Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro Ala		
324	115 120 125		
326	ggg ttg gag gtg tct ggg aag ctg aga gtc gcg ctc agc aac cac ctg	432	
327	Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Ser Asn His Leu		
328	130 135 140		
330	ttg tgg tcc aag ttc aac cag cac cag aca gag atg atc atc act aag	480	
331	Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr Lys		
332	145 150 155 160		
334	caa gga cgg cga atg ttc cca ttc ctg tcc ttc acc gtg gcc ggg ctg	528	
335	Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly Leu		
336	165 170 175		
338	gag ccc aca agc cat tac agg atg ttt gtg gat gtg gtc ttg gtg gac	576	
339	Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val Asp		
340	180 185 190		

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<400> 9

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Attorney Docket No.: HUI-040CP

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VERIFICATION SUMMARY
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DATE: 01/31/2006
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Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\01312006\J008264C.raw

L:600 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:605 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9